==========

Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=7; day=27; hr=9; min=43; sec=57; ms=320;]

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Reviewer Comments:

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<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> n is glycine or alanine.

<220>

<221> misc_feature

<222> (7)..(7)

<223> n is threonine or cysteine.

<220>

<221> misc_feature

<222> (8)..(8)

<223> n is threonine or cysteine.

<400> 57

nggaganntg

10

The above <220>-<223> sections describing the "n's" are errored: "n" can only represent a single nucleotide; it cannot represent an amino

acid.

<210> 130
<211> 10
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<220>
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<222> (1)..(1)
<223> X can be a or g.

<220>
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<223> X can be t or c.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X can be a or g.

<400> 130

Xaa Gly Gly Ala Gly Ala Xaa Thr Thr Xaa
1 5 10

If the above <220>-<223> sections regarding the "Xaa's" are defining them as nucleotides, they are erroneous. If they are denoting amino acids, please spell them out in the <223> responses.
****

Validated By CRFValidator v 1.0.3

Application No: 10574333 Version No: 1.0

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Output Set:

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Input Set:

Output Set:

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Total Warnings: 100
Total Errors: 0
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Actual SeqID Count: 134

Error code	Error Description
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SEQUENCE LISTING

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Karin, Michael
Bonizzi, Giussepina
Bebien, Mahali

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<141> 2010-07-21

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<151> 2003-10-01

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<212> PRT
<213> Homo sapiens

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1 5 10 15

Asp Phe Lys Leu Asn Ser Ser Ile Val Glu Pro Lys Glu Pro Ala Pro
20 25 30

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
35 40 45

Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
50 55 60

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65 70 75 80

Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
85 90 95

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
100 105 110

Gln Cys Ser Glu Leu Gly Ile Cys Ala Val Ser Val Gly Pro Lys Asp
115 120 125

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
130 135 140

Asn Met Met Gly Thr Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145 150 155 160

Ser Arg Pro Gln Gly Leu Thr Glu Ala Glu Gln Arg Glu Leu Glu Gln
165 170 175

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Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
            180                 185                 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
        195                 200                 205

Leu Lys Pro Val Thr Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
    210                 215                 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225                 230                 235                 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
                245                 250                 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
            260                 265                 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
        275                 280                 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
    290                 295                 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305                 310                 315                 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
                325                 330                 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
            340                 345                 350

Gly Ser His Met Gly Gly Gly Ser Gly Gly Ala Ala Gly Gly Tyr Gly
        355                 360                 365

Gly Ala Gly Gly Gly Gly Ser Leu Gly Phe Phe Pro Ser Ser Leu Ala
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Tyr Ser Pro Tyr Gln Ser Gly Ala Gly Pro Met Arg Cys Tyr Pro Gly
385                 390                 395                 400
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Gly Gly Gly Gly Ala Gln Met Ala Ala Thr Val Pro Ser Arg Asp Ser
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Gly Glu Glu Ala Ala Glu Pro Ser Ala Pro Ser Arg Thr Pro Gln Cys
            420                 425                 430

Glu Pro Gln Ala Pro Glu Met Leu Gln Arg Ala Arg Glu Tyr Asn Ala
        435                 440                 445

Arg Leu Phe Gly Leu Ala His Ala Ala Pro Ser Pro Thr Arg Leu Leu
    450                 455                 460

Arg His Arg Gly Arg Arg Ala Leu Leu Ala Gly Gln Arg His Leu Leu
465                 470                 475                 480

Thr Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu Ala Ile Ile
                485                 490                 495

His Gly Gln Thr Ser Val Ile Glu Gln Ile Val Tyr Val Ile His His
            500                 505                 510

Ala Gln Asp Leu Gly Val Val Asn Leu Thr Asn His Leu His Gln Thr
        515                 520                 525

Pro Leu His Leu Ala Val Ile Thr Gly Gln Thr Ser Val Val Ser Phe
    530                 535                 540

Leu Leu Arg Val Gly Ala Asp Pro Ala Leu Leu Asp Arg His Gly Asp
545                 550                 555                 560

Ser Ala Met His Leu Ala Leu Arg Ala Gly Ala Gly Ala Pro Glu Leu
                565                 570                 575

Leu Arg Ala Leu Leu Gln Ser Gly Ala Pro Ala Val Pro Gln Leu Leu
            580                 585                 590

His Met Pro Asp Phe Glu Gly Leu Tyr Pro Val His Leu Ala Val Arg
        595                 600                 605

Ala Arg Ser Pro Glu Cys Leu Asp Leu Leu Val Asp Ser Gly Ala Glu
    610                 615                 620
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Val Glu Ala Thr Glu Arg Gln Gly Gly Arg Thr Ala Leu His Leu Ala
625                 630                 635                 640

Thr Glu Met Glu Glu Leu Gly Leu Val Thr His Leu Val Thr Lys Leu
                645                 650                 655

Arg Ala Asn Val Asn Ala Arg Thr Phe Ala Gly Asn Thr Pro Leu His
            660                 665                 670

Leu Ala Ala Gly Leu Gly Tyr Pro Thr Leu Thr Arg Leu Leu Leu Lys
        675                 680                 685

Ala Gly Ala Asp Ile His Ala Glu Asn Glu Glu Pro Leu Cys Pro Leu
    690                 695                 700

Pro Ser Pro Pro Thr Ser Asp Ser Asp Ser Asp Ser Glu Gly Pro Glu
705                 710                 715                 720

Lys Asp Thr Arg Ser Ser Phe Arg Gly His Thr Pro Leu Asp Leu Thr
                725                 730                 735

Cys Ser Thr Leu Val Lys Thr Leu Leu Leu Asn Ala Ala Gln Asn Thr
            740                 745                 750

Met Glu Pro Pro Leu Thr Pro Pro Ser Pro Ala Gly Pro Gly Leu Ser
        755                 760                 765

Leu Gly Asp Thr Ala Leu Gln Asn Leu Glu Gln Leu Leu Asp Gly Pro
    770                 775                 780

Glu Ala Gln Gly Ser Trp Ala Glu Leu Ala Glu Arg Leu Gly Leu Arg
785                 790                 795                 800

Ser Leu Val Asp Thr Tyr Arg Gln Thr Thr Ser Pro Ser Gly Ser Leu
                805                 810                 815

Leu Arg Ser Tyr Glu Leu Ala Gly Gly Asp Leu Ala Gly Leu Leu Glu
            820                 825                 830

Ala Leu Ser Asp Met Gly Leu Glu Glu Gly Val Arg Leu Leu Arg Gly
        835                 840                 845

Pro Glu Thr Arg Asp Lys Leu Pro Ser Thr Glu Val Lys Glu Asp Ser
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    850                 855                 860

Ala Tyr Gly Ser Gln Ser Val Glu Gln Glu Ala Glu Lys Leu Gly Pro
865                 870                 875                 880

Pro Pro Glu Pro Pro Gly Gly Leu Ser His Gly His Pro Gln Pro Gln
                885                 890                 895

Val Thr Asp Leu Leu Pro Ala Pro Ser Pro Leu Pro Gly Pro Pro Val
            900                 905                 910

Gln Arg Pro His Leu Phe Gln Ile Leu Phe Asn Thr Pro His Pro Pro
        915                 920                 925

Leu Ser Trp Asp Lys
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<211> 3001
<212> DNA
<213> Homo sapiens

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cctggccgga gccactagac agagccgggc ctagcccaga gacatggaga gttgctacaa      180

cccaggtctg gatggtatta ttgaatatga tgatttcaaa ttgaactcct ccattgtgga      240

acccaaggag ccagccccag aaacagctga tggcccctac ctggtgatcg tggaacagcc      300

taagcagaga ggcttccgat ttcgatatgg ctgtgaaggc ccctcccatg gaggactgcc      360

cggtgcctcc agtgagaagg gccgaaagac ctatcccact gtcaagatct gtaactacga      420

gggaccagcc aagatcgagg tggacctggt aacacacagt gacccacctc gtgctcatgc      480

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caaggacatg actgcccaat ttaacaacct gggtgtcctg catgtgacta agaagaacat      600

gatggggact atgatacaaa aacttcagag gcagcggctc cgctctaggc cccagggcct      660

tacggaggcc gagcagcggg agctggagca agaggccaaa gaactgaaga aggtgatgga      720

tctgagtata gtgcggctgc gcttctctgc cttccttaga gccagtgatg gctccttctc      780

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t 3001

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1 5 10 15

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20 25 30

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
35 40 45

Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
50 55 60

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65 70 75 80

Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
85 90 95

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
100 105 110

Gln Cys Ser Glu Leu Gly Val Cys Ala Val Ser Val Gly Pro Lys Asp
115 120 125

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Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
    130                 135                 140

Asn Met Met Glu Ile Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145                 150                 155                 160

Ser Lys Pro Gln Gly Leu Thr Glu Ala Glu Arg Arg Glu Leu Glu Gln
                165                 170                 175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
            180                 185                 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
        195                 200                 205

Leu Lys Pro Val Ile Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
    210                 215                 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225                 230                 235                 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
                245                 250                 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
            260                 265                 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
        275                 280                 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
    290                 295                 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305                 310                 315                 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
                325                 330                 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
            340                 345                 350

Gly Ser His Met Gly Gly Gly Ser Gly Gly Ser Ala Gly Gly Tyr Gly
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        355                 360                 365

Gly Ala Gly Gly Gly Gly Ser Leu Gly Phe Phe Ser Ser Ser Leu Ala
    370                 375                 380

Tyr Asn Pro Tyr Gln Ser Gly Ala Ala Pro Met Gly Cys Tyr Pro Gly
385                 390                 395                 400

Gly Gly Gly Gly Ala Gln Met Ala Gly Ser Arg Arg Asp Thr Asp Ala
                405                 410                 415

Gly Glu Gly Ala Glu Glu Pro Arg Thr Pro Pro Glu Ala Pro Gln Gly
            420                 425                 430

Glu Pro Gln Ala Leu Asp Thr Leu Gln Arg Ala Arg Glu Tyr Asn Ala
        435                 440                 445

Arg Leu Phe Gly Leu Ala Gln Arg Ser Ala Arg Ala Leu Leu Asp Tyr
    450                 455                 460

Gly Val Thr Ala Asp Ala Arg Ala Leu Leu Ala Gly Gln Arg His Leu
465                 470                 475                 480

Leu Met Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu
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